

Appl. No. 09/724,910

Response to Office Action dated 08/09/05

Response dated February 9, 2006

AMENDMENTS

A complete listing and status of the claims is provided below, which replaces all previous listing of the claims. All previous pending claims have been withdrawn. Claims 46-51 have been added.

1. (Withdrawn) A computer-implemented method for making correct allele calls, comprising:
receiving data representing nucleic acid information;
applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and
depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.
2. (Withdrawn) The computer-implemented method of claim 1, wherein the allele calling algorithms applied in the step of applying at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.
3. (Canceled)
4. (Withdrawn) A computer-implemented method for making correct allele calls, comprising:
receiving signal representing nucleic acid information;
applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

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5. (Withdrawn) The method of claim 4, wherein the applying step includes the substeps of:

creating a list of peaks in the signal;
determining characteristics associated with each peak; and
removing peaks from the list based on the determined characteristics.

6. (Canceled)

7. (Withdrawn) A computer-implemented method for interpreting nucleotide or amino acid information, comprising:

receiving data representing nucleotide or amino acid information;
applying at least two different algorithms to the data to provide a result for each algorithm; and
depending on agreement between the results of each algorithms, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result.

8. (Withdrawn) The computer-implemented method of claim 7, wherein the algorithms applied in the step of applying at least two different algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

9 (Withdrawn) A computer-implemented method for making correct allele calls associated with data representing nucleic acid information, comprising:
applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein
each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;
if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

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if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

10. (Withdrawn) The computer-implemented method of claim 9, wherein the allele calling algorithms applied in the applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

11 (Withdrawn) A system for making correct allele calls, comprising:
a processor configured to execute program instructions; and
a memory containing program instructions for execution by the processor to receive data representing nucleic acid information,
apply at least two different allele calling algorithms to the data to provide a result for each algorithm, and
depending on agreement between the results of each algorithm, identify an allele call within the data and assigning a confidence level for each call.

12. (Withdrawn) The computer-implemented method of claim 11, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

13. (Withdrawn) The system of claim 11, wherein the nucleic acid information comprises nucleic acid length.

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14. (Canceled)

15. (Canceled)

16. (Withdrawn) A system for making correct allele calls, comprising:

a processor configured to execute program instructions; and

a memory containing program instructions for execution by the processor to receive signal representing nucleic acid information,

apply a set of filters to the signal to eliminate peaks that do not represent alleles,

wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker, and

determine that remaining peaks in the data are alleles after applying the set of filters to the signal.

17. (Withdrawn) The system of claim 16, wherein when the processor executing program instructions applies the set of filters to the signal to eliminate peaks that do not represent alleles,

the processor creates a list of peaks in the signal, determines characteristics associated with each peak, and removes peaks from the list based on the determined characteristics.

18. (Withdrawn) The system of claim 16, wherein the nucleic acid information comprises nucleic acid length.

19 (Withdrawn) A system for interpreting nucleotide or amino acid information, comprising:

a processor to execute program instructions; and

a memory that stores program instructions for execution by the processor to receive data representing nucleotide or amino acid information,

apply at least two different algorithms to the data to provide a result for each algorithm, and

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depending on agreement between the results of each algorithm, identify at least one correct result within the data and assigning a confidence level to the at least one correct result.

20. (Withdrawn) The system of claim 19, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

21. (Withdrawn) A system for making correct allele calls associated with data representing nucleic acid information, comprising:
a processor to execute program instructions; and
a memory that stores program instructions for execution by the processor to apply each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data,
if results from all of the applied allele calling algorithms are consistent, assign a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms,
if results from all of the applied allele calling algorithms are not consistent, assign different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results, and
output a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data

22. (Withdrawn) The system of claim 21, wherein the allele calling algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

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23. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:
receiving data representing nucleic acid information;
applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and
depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

24. (Withdrawn) The computer readable medium of claim 23, wherein the allele calling algorithms applied in the applying of at least two different allele calling algorithms to the data to provide a result for each algorithm are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

25. (Cancelled)

26. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls, the method comprising:
receiving signal representing nucleic acid information;
applying a set of filters to the signal to eliminate peaks that do not represent alleles, wherein the set of filters include at least one of the following: a split peak checker; a background peak checker; a shoulder peak checker; a spike peak checker; a special peak checker; and a one basepair checker; and
determining that remaining peaks in the data are alleles after applying the set of filters to the signal.

27. (Withdrawn) The computer readable medium of claim 26, wherein the applying of the set of filters includes:
creating a list of peaks in the signal;
determining characteristics associated with each peak; and

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removing peaks from the list based on the determined characteristics.

28. (Canceled)

29. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for interpreting nucleotide or amino acid information, the method comprising:
receiving data representing nucleotide or amino acid information;
applying at least two different algorithms to the data to provide a result for each algorithm; and
depending on agreement between the results of each algorithm, identifying at least one correct result within the data and assigning a confidence level to the at least one correct result, applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;
if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms.

30. (Withdrawn) The computer readable medium of claim 29, wherein the algorithms applied are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

31. (Withdrawn) A computer readable medium containing instructions for controlling a computer system to perform a method for making correct allele calls associated with data representing nucleic acid information, the method comprising:
applying each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data;

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if results from all of the applied allele calling algorithms are consistent, assigning a high level of confidence for any allele calls identified in the data during application of the allele calling algorithms;

if results from all of the applied allele calling algorithms are not consistent, assigning different levels of confidence for any allele calls identified in the data during application of the allele calling algorithms depending upon which combination of the applied allele calling algorithms share consistent results; and

outputting a report including information associated with the results and any assignment of confidence levels for any allele calls identified in the data.

32. (Withdrawn) The computer readable medium of claim 31, wherein the allele calling algorithms applied in the applying of each one of a plurality of allele calling algorithms to data representing nucleic acid information to determine whether there are any allele calls represented in the data, wherein each allele calling algorithm applies a different strategy in determining whether there is an allele call represented in the data, are selected from an envelope detection caller algorithm, an optimizer caller algorithm, and a heuristic caller algorithm.

33. (Withdrawn) A system for making correct allele calls, comprising:

means for receiving data representing nucleic acid information;

means for applying at least two different allele calling algorithms to the data to provide a result for each algorithm; and

means for depending on agreement between the results of each algorithm, identifying an allele call within the data and assigning a confidence level for each call.

34. (Withdrawn) A computer-implemented method for processing a signal, comprising:

receiving the signal representing nucleic acid information;

analyzing the signal to determine if the signal meets a threshold test of an allele caller

making a correct call; and

making an allele call for the signal if the threshold test is met.

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35. (Withdrawn) The method of claim 34, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy level information, and wherein the nucleic acid length, panel determination, and energy level information are used for analyzing the signal.

36. (Withdrawn) The method of claim 35, wherein analyzing the nucleic acid information includes:
determining if at least three panels exist in the signal; and
if at least three panels exist, computing an energy level for each panel.

37. (Withdrawn) The method of claim 36, wherein making an allele call includes:
comparing the computed energy levels of the panels to determine if the threshold test is met.

38. (Withdrawn) A system for processing a signal, comprising:
a memory containing program instructions; and
a processor configured to execute the program instructions in the memory and to:
receive the signal representing nucleic acid information;
analyze the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and
make an allele call for the signal if the threshold test is met.

39. (Withdrawn) The system of claim 38, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy level information, and wherein the nucleic acid length, panel determination, and energy level information are used for analyzing the signal.

40. (Withdrawn) The system of claim 39, wherein the processor is further

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configured to determine if at least three panels exist in the signal, and if at least three panels exist, compute an energy level for each panel.

41. (Withdrawn) The system of claim 40, wherein the processor is further configured to compare the computed energy levels of the panels to determine if the threshold test is met.

42 (Withdrawn) A computer-readable medium containing instructions for controlling a computer system to perform a method for processing a signal, the method comprising:
receiving the signal representing nucleic acid information;
analyzing the signal to determine if the signal meets a threshold test of an allele caller making a correct call; and
making an allele call for the signal if the threshold test is met.

43. (Withdrawn) The computer-readable medium of claim 42, wherein the nucleic acid information is used to determine nucleic acid length, panel determination, and energy level information, and wherein the nucleic acid length, panel determination, and energy level information are used for analyzing the signal.

44. (Withdrawn). The computer-readable medium of claim 43, wherein the computer system is to further perform a method comprising:
determining if at least three panels exist in the signal; and
if at least three panels exist, computing an energy level for each panel,

45. (Withdrawn) The computer-readable medium of claim 44, wherein the computer system is to further perform a method comprising:
comparing the computed energy levels of the panels to determine if the threshold test is met.

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46. (New) A method for processing fragment analysis data, comprising:

- receiving the fragment analysis data wherein the data represents intensity and nucleic acid fragment length information,
- presenting the fragment analysis data to a two-stage allele caller ,
 - wherein a second stage is configured to perform a second analysis that determines allele calls for the fragment analysis data and a first stage is configured to perform a first analysis to determine whether or not the fragment analysis data signal is within the second stage's operating region,
- performing said first analysis with said first stage and if said first stage determines that said fragment analysis data is within said second stage's operating region, performing said second analysis, and
- reporting the results of said first and second analysis.

47. (New) The method of claim 46 wherein said first stage is configured to determine one or more maxima of said fragment analysis data and form a first signal composed of the one or more maxima, to determine one or more minima of said first signal and to divide said first signal into one or more panels with a panel boundary located at each of the one or more minima, and then to determine if three or more panels exist.

48. (New) The method of claim 47 wherein said second stage is configured to perform said second analysis if at least three panels exist wherein said second analysis comprises:

- determining the energy in each panel,
- defining a first panel corresponding to the panel which contains the greatest energy,
- defining a second panel corresponding to the panel which contains the second greatest energy,
- defining a third panel corresponding to the panel which contains the third greatest energy,

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- performing a first test to determine if the ratio of the energy in the first panel to the energy in the second panel is above a first threshold,
- performing a second test to determine if the ratio of the energy in the third panel to the energy in the second panel is below a second threshold, and
- calling alleles in each of the first and second panels if the first and second tests are passed.

49. (New) The method of claim 48 wherein said calling alleles step comprises:

- defining a first allele in the first panel as the fragment length corresponding to the maximum intensity value in the first panel, and
- defining a second allele in the second panel as the fragment length corresponding to the maximum intensity value in the second panel.

50. (New) The method of claim 48 wherein energy is defined as the integral of the signal contained in the panel.

51. (New) A computer readable medium containing instructions for controlling a computer system to perform a method for processing fragment analysis data, the method comprising:

- receiving the fragment analysis data wherein the data represents intensity and nucleic acid fragment length information,
- presenting the fragment analysis data to a two-stage allele caller,
 - wherein a second stage is configured to perform a second analysis that determines allele calls for the fragment analysis data and a first stage is configured to perform a first analysis to determine whether or not the fragment analysis data signal is within the second stage's operating region,
- performing said first analysis with said first stage and if said first stage determines that said fragment analysis data is within said second stage's operating region, performing said second analysis, and
- reporting the results of said first and second analysis.